

# wwPDB X-ray Structure Validation Summary Report (i)

#### May 17, 2020 - 04:47 am BST

PDB ID	:	6HUL
Title	:	Sulfolobus solfataricus Tryptophan Synthase AB Complex
Authors	:	Fleming, J.R.; Mayans, O.
Deposited on	:	2018-10-08
Resolution	:	2.55  Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org A user guide is available at https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

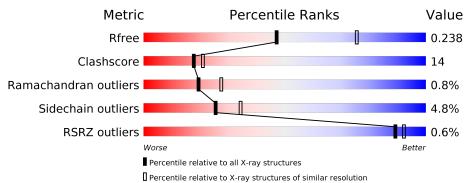
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	$7.0.044 (\mathrm{Gargrove})$
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
$R_{free}$	130704	$1284 \ (2.56-2.52)$
Clashscore	141614	1332(2.56-2.52)
Ramachandran outliers	138981	1315(2.56-2.52)
Sidechain outliers	138945	1315(2.56-2.52)
RSRZ outliers	127900	1272(2.56-2.52)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain		
1	А	241	% 70%	29%	-
2	В	425	70%	24% •	•

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:



Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	G3P	А	301	Х	-	-	-
4	SER	В	501[A]	-	-	-	Х
4	SER	В	501[B]	-	-	-	Х



# 2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 5330 atoms, of which 1 is hydrogen and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

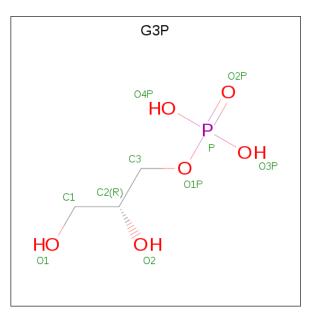
• Molecule 1 is a protein called Tryptophan synthase alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	А	241	Total 1902	C 1243	N 304	O 351	$\frac{S}{4}$	0	1	0

• Molecule 2 is a protein called Tryptophan synthase beta chain 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
2	В	416	Total 3324	С 2143	H 1	N 560	O 610	S 10	0	3	0

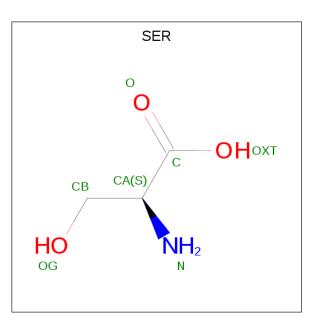
• Molecule 3 is SN-GLYCEROL-3-PHOSPHATE (three-letter code: G3P) (formula:  $C_3H_9O_6P$ ).



Mol	Chain	Residues	Atc	ms		ZeroOcc	AltConf
3	А	1	Total C 10 3	0 6	Р 1	0	0

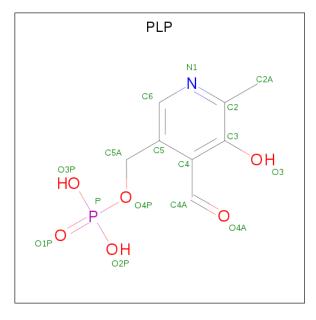
• Molecule 4 is SERINE (three-letter code: SER) (formula:  $C_3H_7NO_3$ ).





]	Mol	Chain	Residues	A	ton	ns		ZeroOcc	AltConf
	4	В	1	Total 14	С 6	N 2	O 6	0	1

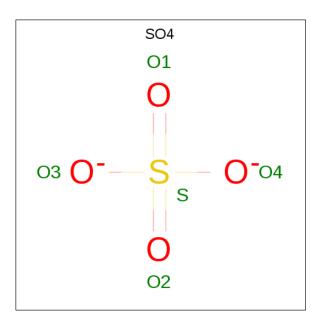
• Molecule 5 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula:  $C_8H_{10}NO_6P$ ).



Mol	Chain	Residues		Ate	oms			ZeroOcc	AltConf
E E	р	1	Total	С	Ν	0	Р	0	0
5	D	T	15	8	1	5	1	0	0

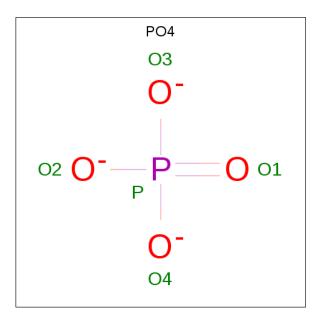
 $\bullet\,$  Molecule 6 is SULFATE ION (three-letter code: SO4) (formula:  ${\rm O_4S}).$ 





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
6	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
6	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0

• Molecule 7 is PHOSPHATE ION (three-letter code: PO4) (formula:  $O_4P$ ).



B	1	Total 5	O $4$	Р 1	0	0

Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{P} \\ 5 & 4 & 1 \end{array}$	0	0
7	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{P} \\ 5 & 4 & 1 \end{array}$	0	0

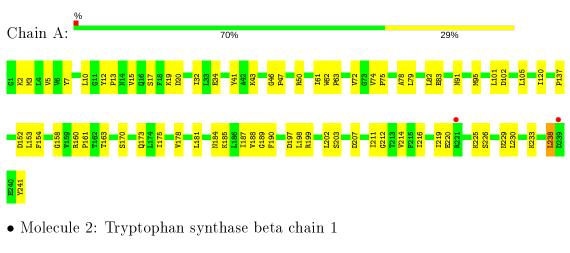
• Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	А	7	Total O 7 7	0	0
8	В	28	Total         O           28         28	0	0

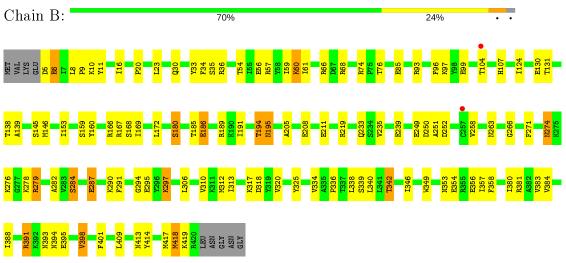


# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.



• Molecule 1: Tryptophan synthase alpha chain





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants	128.98Å 128.98Å 217.37Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	34.46 - 2.55	Depositor
Resolution (A)	34.46 - 2.50	EDS
% Data completeness	99.6 (34.46-2.55)	Depositor
(in resolution range)	99.0(34.46-2.50)	EDS
R <sub>merge</sub>	0.15	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.05 (at 2.51 \text{\AA})$	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
D D.	0.182 , $0.239$	Depositor
$R, R_{free}$	0.182 , $0.238$	DCC
$R_{free}$ test set	1863 reflections $(5.00\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	54.1	Xtriage
Anisotropy	0.191	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.33 , $35.7$	EDS
L-test for twinning <sup>2</sup>	$ \langle L  \rangle = 0.50, \langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5330	wwPDB-VP
Average B, all atoms $(Å^2)$	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.40% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 5 Model quality (i)

### 5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: G3P, PO4, SO4, PLP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 5 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol Chain		Bond	lengths	Bond angles	
	Cham	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.41	0/1940	0.58	0/2629
2	В	0.45	0/3410	0.62	0/4621
All	All	0.44	0/5350	0.61	0/7250

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	<b>#Planarity outliers</b>
2	В	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	$\mathbf{Res}$	Type	Group
2	В	6	GLU	Peptide

### 5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	1902	0	1988	57	0
2	В	3323	1	3357	91	0
3	А	10	0	7	1	0
4	В	14	0	8	1	0
5	В	15	0	7	1	0
6	В	15	0	0	0	0
7	В	15	0	0	0	0
8	А	7	0	0	0	0
8	В	28	0	0	3	0
All	All	5329	1	5367	145	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 14.

The worst 5 of 145 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:418:MET:O	8:B:601:HOH:O	1.81	0.96
2:B:131:THR:OG1	4:B:501[A]:SER:OXT	1.94	0.85
2:B:276:LYS:NZ	8:B:602:HOH:O	2.11	0.82
1:A:62:TRP:CZ3	1:A:95[B]:MET:HG3	2.15	0.81
1:A:202:LEU:HD11	1:A:238:LEU:HD22	1.64	0.79

There are no symmetry-related clashes.

### 5.3 Torsion angles (i)

#### 5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentile
1	А	240/241~(100%)	229~(95%)	10~(4%)	1 (0%)	34 46
2	В	417/425~(98%)	401 (96%)	12 (3%)	4 (1%)	15 22
All	All	657/666~(99%)	630~(96%)	22 (3%)	5(1%)	19 27



All (5) Ramachandran outliers are listed below:

Mol	Chain	$\mathbf{Res}$	Type
2	В	419	LYS
2	В	279	ARG
2	В	394	ASN
1	А	212	GLY
2	В	195	ASN

#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	213/212~(100%)	208~(98%)	5(2%)	50 65
2	В	355/359~(99%)	333~(94%)	22~(6%)	18 24
All	All	568/571~(100%)	541 (95%)	27~(5%)	25 34

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	В	180	SER
2	В	194	THR
2	В	395	GLU
2	В	186	GLU
1	А	238	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	В	216	ASN

#### 5.3.3 RNA (i)

There are no RNA molecules in this entry.



#### 5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

#### 5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

### 5.6 Ligand geometry (i)

10 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Tune	Chain	Res	Link	Bo	ond leng	ths	В	ond ang	les
	Type	Cham	nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	#  Z  > 2
6	SO4	В	504	-	$4,\!4,\!4$	0.17	0	6, 6, 6	0.27	0
6	SO4	В	505	-	$4,\!4,\!4$	0.19	0	$6,\!6,\!6$	0.13	0
7	PO4	В	507	-	$4,\!4,\!4$	0.89	0	$6,\!6,\!6$	0.46	0
6	SO4	В	503	-	4,4,4	0.17	0	$6,\!6,\!6$	0.54	0
3	G3P	А	301	-	$9,\!9,\!9$	0.59	0	$11,\!12,\!12$	1.15	1 (9%)
5	PLP	В	502	2	15, 15, 16	2.43	7 (46%)	$20,\!22,\!23$	1.09	1(5%)
7	PO4	В	508	-	$4,\!4,\!4$	0.78	0	$6,\!6,\!6$	0.61	0
7	PO4	В	506	-	$4,\!4,\!4$	0.80	0	$6,\!6,\!6$	0.68	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PLP	В	502	2	-	0/6/6/8	0/1/1/1
3	G3P	А	301	-	1/1/2/2	7/8/8/8	-

The worst 5 of 7 bond length outliers are listed below:



Mol	Chain	$\mathbf{Res}$	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
5	В	502	PLP	C4A-C4	5.64	1.63	1.51
5	В	502	PLP	C2A-C2	3.55	1.56	1.50
5	В	502	PLP	C5-C4	-2.87	1.37	1.40
5	В	502	PLP	C3-C2	2.70	1.43	1.40
5	В	502	PLP	C6-N1	2.59	1.39	1.34

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	А	301	G3P	O4P-P-O1P	2.66	113.81	106.73
5	В	502	PLP	C6-C5-C4	2.12	119.82	118.16

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	А	301	G3P	C2

5 of 7 torsion outliers are listed below:

Mol	Chain	$\mathbf{Res}$	Type	Atoms
3	А	301	G3P	C3-O1P-P-O4P
3	А	301	G3P	C3-O1P-P-O2P
3	А	301	G3P	C3-O1P-P-O3P
3	А	301	G3P	C1-C2-C3-O1P
3	А	301	G3P	O2-C2-C3-O1P

There are no ring outliers.

2 monomers are involved in 2 short contacts:

$\mathbf{Mol}$	Chain	$\mathbf{Res}$	Type	Clashes	Symm-Clashes
3	А	301	G3P	1	0
5	В	502	PLP	1	0

### 5.7 Other polymers (i)

There are no such residues in this entry.

### 5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



# 6 Fit of model and data (i)

## 6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ $>$	#RSRZ>2		$OWAB(Å^2)$	Q<0.9	
1	А	241/241~(100%)	-0.31	2 (0%)	86	89	42, 56, 82, 109	0
2	В	416/425~(97%)	-0.30	2 (0%)	91	94	35, 48, 72, 103	0
All	All	657/666~(98%)	-0.31	4 (0%)	89	92	35, 51, 77, 109	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	221	ARG	2.9
1	А	239	ASP	2.7
2	В	257	CYS	2.4
2	В	104[A]	THR	2.2

## 6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

## 6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median,  $95^{th}$  percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	Q<0.9
4	SER	В	501[B]	7/7	0.76	0.64	42,46,48,49	7

Continued on next page...



Mol	Type	Chain	Res	Atoms	RSCC	$\mathbf{RSR}$	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	$\mathbf{Q}{<}0.9$
4	SER	В	501[A]	7/7	0.76	0.64	$35,\!39,\!47,\!48$	7
7	PO4	В	507	5/5	0.79	0.19	107,111,114,118	0
7	PO4	В	508	5/5	0.88	0.26	$109,\!111,\!114,\!115$	0
6	SO4	В	505	5/5	0.90	0.46	106, 106, 111, 114	0
7	PO4	В	506	5/5	0.90	0.39	109,109,111,115	0
6	SO4	В	504	5/5	0.93	0.19	$108,\!108,\!110,\!115$	0
3	G3P	А	301	10/10	0.95	0.26	51,59,72,74	0
6	SO4	В	503	5/5	0.99	0.15	70,71,72,79	0
5	PLP	В	502	15/16	0.99	0.25	$36,\!50,\!67,\!69$	0

Continued from previous page...

## 6.5 Other polymers (i)

There are no such residues in this entry.

